



SEQUENCE LISTING

<110> Roberts, Shannon
Sherman, Amir
Trueheart, Joshua
Milne, G. Todd

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Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65 70 75 80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130 135 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145 150 155 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165 170 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180 185 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195 200 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210 215 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225 230 235 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys Arg Gln Gly Thr
245 250 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260 265 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275 280 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290 295 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Pro Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350
Ala Cys Thr Thr Leu His Val Gln Leu Leu Arg Glu Asn Glu

355	360	365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser		
370	375	380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn		
385	390	395
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu		
405	410	415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala		
420	425	430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp		
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20	25	30
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35	40	45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly		
50	55	60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln		
65	70	75
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His		
85	90	95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser		
100	105	110
Glu Ser His Ser Ser Asn Thr Ser Trp Gln Phe Leu Asp Pro Pro Asp		
115	120	125
Ser Tyr Asp Trp Leu Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp		
130	135	140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln		
145	150	155
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val		
165	170	175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala		
180	185	190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu		
195	200	205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu		
210	215	220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu		
225	230	235
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr		
245	250	255

Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Gly
 305 310 315 320
 His Gly Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
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 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Val Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
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Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
      35          40          45

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Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
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 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Gly Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
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 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
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 Asn Asn Ile Pro Pro
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Arg	Ser	Cys	Asp	Arg	Cys	His	Ala	Gln	Lys	Ile	Lys	Cys	Thr	Gly	Asn
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Lys	Glu	Val	Thr	Gly	Arg	Ala	Pro	Cys	Gln	Arg	Cys	Gln	Gln	Ala	Gly
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Leu	Arg	Cys	Val	Tyr	Ser	Glu	Arg	Arg	Pro	Lys	Arg	Lys	Leu	Arg	Gln
	65							70			75		80		
Ser	Arg	Ala	Ala	Asp	Leu	Val	Ser	Ala	Asp	Pro	Asp	Pro	Cys	Leu	His
								85			90		95		
Met	Ser	Ser	Pro	Pro	Val	Pro	Ser	Gln	Ser	Leu	Pro	Leu	Asp	Val	Ser
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Glu	Ser	His	Ser	Ser	Asn	Thr	Ser	Arg	Gln	Phe	Leu	Asp	Pro	Pro	Asp
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Ser	Tyr	Asp	Trp	Ser	Trp	Thr	Ser	Ile	Gly	Thr	Asp	Glu	Ala	Ile	Asp
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Thr	Asp	Cys	Trp	Gly	Leu	Ser	Gln	Cys	Asp	Gly	Gly	Phe	Ser	Cys	Gln
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Leu	Glu	Pro	Thr	Leu	Pro	Asp	Leu	Pro	Ser	Pro	Phe	Glu	Ser	Thr	Val
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Glu	Lys	Ala	Pro	Leu	Pro	Pro	Val	Ser	Ser	Asp	Ile	Ala	Arg	Ala	Ala
								180			185		190		
Ser	Ala	Gln	Arg	Glu	Leu	Phe	Asp	Asp	Leu	Ser	Ala	Val	Ser	Gln	Glu
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Ile	Trp	Thr	His	Pro	Ile	Gly	Met	Phe	Phe	Asn	Ala	Ser	Arg	Arg	Leu
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Tyr	Ile	Leu	Asn	Val	Arg	Ile	Leu	Thr	Ala	Ile	Ser	Glu	Leu	Leu	Leu
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His	Ser	Ser	Val	Asp	Thr	Ile	Pro	Phe	Phe	Ser	Glu	Asn	Leu	Pro	Ile
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Gly	Glu	Leu	Phe	Ser	Tyr	Val	Asp	Pro	Leu	Thr	His	Ala	Leu	Phe	Ser
								340			345		350		
Ala	Cys	Thr	Thr	Leu	His	Val	Gly	Val	Gln	Leu	Leu	Arg	Glu	Asn	Glu
								355			360		365		
Ile	Thr	Leu	Gly	Val	His	Ser	Ala	Gln	Gly	Ile	Ala	Ala	Ser	Ile	Ser
								370			375		380		
Met	Ser	Gly	Glu	Pro	Gly	Glu	Asp	Ile	Ala	Arg	Thr	Gly	Ala	Thr	Asn
	385							390			395		400		

Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
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 Asn Asn Ile Pro Pro
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<220>
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 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Tyr Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Lys Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly

290	295	300	
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly			
305	310	315	320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile			
325	330	335	
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser			
340	345	350	
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu			
355	360	365	
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser			
370	375	380	
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn			
385	390	395	400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu			
405	410	415	
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala			
420	425	430	
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp			
435	440	445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu			
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Asn Asn Ile Pro Pro			
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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 47

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro			
1	5	10	15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg			
20	25	30	
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln			
65	70	75	80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp			
130	135	140	
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln			
145	150	155	160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val			
165	170	175	
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala			
180	185	190	

Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Ser Ile Pro Pro
 465

<210> 48
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 48
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His

85	90	95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser		
100	105	110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp		
115	120	125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp		
130	135	140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln		
145	150	155
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val		
165	170	175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala		
180	185	190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu		
195	200	205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu		
210	215	220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu		
225	230	235
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala		
245	250	255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys		
260	265	270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu		
275	280	285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly		
290	295	300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly		
305	310	315
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile		
325	330	335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser		
340	345	350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu		
355	360	365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser		
370	375	380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn		
385	390	395
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu		
405	410	415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala		
420	425	430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp		
435	440	445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu		
450	455	460
Asn Ser Ile Pro Pro		
465		

<210> 49

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 49

Met	Ala	Ala	Asp	Gln	Gly	Ile	Phe	Thr	Asn	Ser	Val	Thr	Leu	Ser	Pro
1				5					10				15		
Val	Glu	Gly	Ser	Arg	Thr	Gly	Gly	Thr	Leu	Pro	Arg	Arg	Ala	Phe	Arg
				20				25				30			
Arg	Ser	Cys	Asp	Arg	Cys	His	Ala	Gln	Lys	Ile	Lys	Cys	Thr	Gly	Asn
				35				40			45				
Lys	Glu	Val	Thr	Gly	Arg	Ala	Pro	Cys	Gln	Arg	Cys	Gln	Gln	Ala	Gly
				50				55			60				
Leu	Arg	Cys	Val	Tyr	Ser	Glu	Arg	Arg	Pro	Lys	Arg	Lys	Leu	Arg	Gln
65					70				75			80			
Ser	Arg	Ala	Ala	Asp	Leu	Val	Ser	Ala	Asp	Pro	Asp	Pro	Cys	Leu	His
				85				90			95				
Met	Ser	Ser	Pro	Pro	Val	Pro	Ser	Gln	Ser	Leu	Pro	Leu	Asp	Val	Ser
				100				105			110				
Glu	Ser	His	Ser	Ser	Asn	Thr	Ser	Arg	Gln	Phe	Leu	Asp	Pro	Pro	Asp
				115				120			125				
Ser	Tyr	Asp	Trp	Ser	Trp	Thr	Ser	Ile	Gly	Thr	Asp	Glu	Ala	Ile	Asp
				130				135			140				
Thr	Asp	Cys	Trp	Gly	Leu	Ser	Gln	Cys	Asp	Gly	Gly	Phe	Ser	Cys	Gln
145					150				155			160			
Leu	Glu	Pro	Thr	Leu	Pro	Asp	Leu	Pro	Ser	Pro	Phe	Glu	Ser	Thr	Val
				165				170			175				
Glu	Lys	Ala	Pro	Leu	Pro	Pro	Val	Ser	Ser	Asp	Ile	Ala	Arg	Ala	Ala
				180				185			190				
Ser	Ala	Gln	Arg	Glu	Leu	Phe	Asp	Asp	Leu	Ser	Ala	Val	Ser	Gln	Glu
				195				200			205				
Leu	Glu	Glu	Ile	Leu	Leu	Ala	Val	Thr	Val	Glu	Trp	Pro	Lys	Gln	Glu
				210				215			220				
Ile	Trp	Thr	His	Pro	Ile	Gly	Met	Phe	Phe	Asn	Ala	Ser	Arg	Arg	Leu
225					230				235			240			
Leu	Thr	Val	Leu	Arg	Gln	Gln	Ala	Gln	Ala	Asp	Cys	His	Gln	Gly	Ala
				245				250			255				
Leu	Asp	Glu	Cys	Leu	Arg	Thr	Lys	Asn	Leu	Phe	Thr	Ala	Val	His	Cys
				260				265			270				
Tyr	Ile	Leu	Asn	Val	Arg	Ile	Leu	Thr	Ala	Ile	Ser	Glu	Leu	Leu	Leu
				275				280			285				
Ser	Gln	Ile	Arg	Arg	Thr	Gln	Asn	Ser	His	Met	Ser	Pro	Leu	Glu	Gly
				290				295			300				
Ser	Arg	Ser	Gln	Ser	Pro	Ser	Arg	Asp	Asp	Thr	Ser	Ser	Ser	Ser	Gly
305					310				315			320			
His	Ser	Ser	Val	Asp	Thr	Ile	Pro	Phe	Phe	Ser	Glu	Asn	Leu	Pro	Ile
				325				330			335				
Gly	Glu	Leu	Phe	Ser	Tyr	Val	Asp	Pro	Leu	Thr	His	Ala	Leu	Phe	Ser
				340				345			350				
Ala	Cys	Thr	Thr	Leu	His	Val	Gly	Val	Gln	Leu	Leu	Arg	Glu	Asn	Glu
				355				360			365				
Ile	Thr	Leu	Gly	Val	His	Ser	Ala	Gln	Gly	Ile	Ala	Ala	Ser	Ile	Ser
				370				375			380				
Met	Ser	Gly	Glu	Pro	Gly	Glu	Asp	Ile	Ala	Arg	Thr	Gly	Ala	Thr	Asn
385					390				395			400			
Ser	Ala	Arg	Cys	Glu	Glu	Gln	Pro	Thr	Thr	Pro	Ala	Ala	Arg	Val	Leu
				405				410			415				
Phe	Met	Phe	Leu	Ser	Asp	Glu	Gly	Ala	Phe	Gln	Glu	Ala	Lys	Ser	Ala
				420				425			430				
Gly	Ser	Arg	Gly	Arg	Thr	Ile	Ala	Ala	Leu	Arg	Arg	Cys	Tyr	Glu	Asp

435	440	445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met	Leu Arg Asp Leu		
450	455	460	
Asn Ser Ile Pro Pro			
465			
<210> 50			
<211> 469			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> synthetically generated variant			
<400> 50			
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro			
1	5	10	15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg			
20	25	30	
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln			
65	70	75	80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp			
130	135	140	
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln			
145	150	155	160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val			
165	170	175	
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala			
180	185	190	
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu			
195	200	205	
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu			
210	215	220	
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu			
225	230	235	240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala			
245	250	255	
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys			
260	265	270	
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu			
275	280	285	
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly			
290	295	300	
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly			
305	310	315	320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile			
325	330	335	

Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Ser Ile Pro Pro
 465

<210> 51

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 51

Met Ala Ala Asp Gln Gly Ile Phe Met Asn Ser Val Thr Leu Ser Ala
 1 5 10 15
 Val Glu Gly Ser Arg Thr Ser Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Lys Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu

225	230	235	240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr			
245	250	255	
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys			
260	265	270	
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu			
275	280	285	
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly			
290	295	300	
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly			
305	310	315	320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile			
325	330	335	
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser			
340	345	350	
Ala Cys Thr Thr Leu His Val Gly Val Glu Leu Leu Arg Glu Asn Glu			
355	360	365	
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser			
370	375	380	
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn			
385	390	395	400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu			
405	410	415	
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala			
420	425	430	
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp			
435	440	445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu			
450	455	460	
Asn Asn Ile Pro Pro			
465			

<210> 52

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 52

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro			
1	5	10	15
Val Glu Gly Ser His Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg			
20	25	30	
Arg Ala Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg His			
65	70	75	80
Ser Arg Ala Ser Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	

Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Asp Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 ~ 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val Asp Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Thr Val Leu Arg Arg Ser Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Ser
 465

<210> 53
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 53
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg

20	25	30	
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln			
65	70	75	80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp			
130	135	140	
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln			
145	150	155	160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val			
165	170	175	
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala			
180	185	190	
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu			
195	200	205	
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu			
210	215	220	
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu			
225	230	235	240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr			
245	250	255	
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys			
260	265	270	
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu			
275	280	285	
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly			
290	295	300	
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly			
305	310	315	320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile			
325	330	335	
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser			
340	345	350	
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu			
355	360	365	
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser			
370	375	380	
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn			
385	390	395	400
Ser Ala Arg Cys Glu Glu Gln Pro Ile Thr Pro Ala Ala Arg Val Leu			
405	410	415	
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala			
420	425	430	
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp			
435	440	445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu			
450	455	460	
Asn Asn Ile Pro Pro			
465			

<210> 54
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 54
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Ile Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Asp Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asn Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Ser Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Ile Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser

370	375	380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn		
385	390	395
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu		400
405	410	415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala		
420	425	430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp		
435	440	445
Ile Phe Ser Leu Ala Arg Lys His Lys Tyr Gly Met Leu Arg Asp Leu		
450	455	460
Asn Asn Ile Pro Pro		
465		

<210> 55

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 55

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro			
1	5	10	15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg			
20	25	30	
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Val Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln			
65	70	75	80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp			
130	135	140	
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln			
145	150	155	160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val			
165	170	175	
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala			
180	185	190	
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu			
195	200	205	
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu			
210	215	220	
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu			
225	230	235	240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr			
245	250	255	
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys			
260	265	270	

Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Leu Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro Cys
 465 470

<210> 56

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 56

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Ser Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Arg Asp Gly Gly Phe Ser Ser Gln
 145 150 155 160
 Leu Lys Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val

	165		170		175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala					
180		185		190	
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu					
195		200		205	
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu					
210		215		220	
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu					
225		230		235	
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr					
245		250		255	
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys					
260		265		270	
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu					
275		280		285	
Ser Gln Ile Arg Leu Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly					
290		295		300	
Ser Arg Ser Gln Ser Pro Asn Arg Asp Asp Thr Ser Ser Ser Ser Gly					
305		310		315	
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile					
325		330		335	
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser					
340		345		350	
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu					
355		360		365	
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser					
370		375		380	
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn					
385		390		395	
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu					
405		410		415	
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala					
420		425		430	
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp					
435		440		445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu					
450		455		460	
Asn Asn Ile Pro Pro					
465					

<210> 57
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

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<400> 57
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Ile Ser Pro
      1           5           10           15
Val Val Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
      20          25          30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
      35          40          45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
      50          55          60

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Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Cys Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Gly Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Leu Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Ser Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Ser
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 58
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 58

Met	Ala	Ala	Asp	Gln	Gly	Ile	Phe	Thr	Asn	Ser	Val	Thr	Leu	Ser	Pro
1				5				10					15		
Val	Glu	Gly	Ser	Arg	Thr	Gly	Gly	Thr	Leu	Pro	Arg	Arg	Ala	Phe	Arg
					20			25					30		
Arg	Ser	Cys	Asp	Arg	Cys	His	Ala	Arg	Lys	Ile	Lys	Cys	Thr	Gly	Asn
						35		40				45			
Lys	Glu	Val	Thr	Gly	Arg	Ala	Pro	Cys	Gln	Arg	Cys	Gln	Gln	Ala	Gly
						50		55				60			
Leu	Arg	Cys	Val	Tyr	Ser	Glu	Arg	Cys	Pro	Lys	Arg	Lys	Leu	Arg	Gln
						65		70			75			80	
Ser	Arg	Ala	Ala	Asp	Leu	Val	Ser	Ala	Asp	Pro	Asp	Pro	Cys	Leu	His
						85			90				95		
Met	Ser	Ser	Pro	Pro	Val	Pro	Ser	Gln	Ser	Leu	Pro	Leu	Asp	Val	Ser
						100		105				110			
Glu	Ser	His	Ser	Ser	Asn	Thr	Ser	Arg	Gln	Phe	Leu	Asp	Pro	Pro	Asp
						115		120				125			
Ser	Tyr	Asp	Trp	Ser	Trp	Thr	Ser	Ile	Gly	Thr	Asp	Glu	Ala	Ile	Asp
						130		135			140				
Thr	Asp	Cys	Trp	Gly	Leu	Ser	Gln	Cys	Asp	Gly	Gly	Phe	Ser	Cys	Gln
						145		150			155			160	
Leu	Glu	Pro	Thr	Leu	Pro	Asp	Leu	Pro	Ser	Pro	Phe	Glu	Tyr	Thr	Val
						165			170			175			
Glu	Lys	Ala	Pro	Leu	Pro	Pro	Val	Ser	Ser	Asp	Ile	Ala	Arg	Ala	Ala
						180			185			190			
Ser	Ala	Gln	Arg	Glu	Leu	Phe	Asp	Asp	Leu	Ser	Ala	Val	Ser	Gln	Glu
						195		200			205				
Leu	Glu	Glu	Ile	Leu	Leu	Ala	Val	Thr	Val	Glu	Trp	Pro	Lys	Gln	Glu
						210		215			220				
Ile	Trp	Thr	His	Pro	Ile	Gly	Met	Phe	Phe	Asn	Ala	Ser	Arg	Arg	Leu
						225		230			235			240	
Leu	Thr	Val	Leu	Arg	Gln	Gln	Ala	Gln	Ala	Asp	Cys	His	Gln	Gly	Thr
						245			250			255			
Leu	Asp	Glu	Cys	Leu	Arg	Thr	Lys	Asn	Leu	Phe	Thr	Ala	Val	His	Cys
						260			265			270			
Tyr	Ile	Leu	Asn	Val	Arg	Ile	Leu	Thr	Ala	Ile	Ser	Glu	Leu	Leu	Leu
						275		280			285				
Ser	Gln	Ile	Arg	Arg	Thr	Gln	Asn	Ser	His	Met	Ser	Pro	Leu	Glu	Gly
						290		295			300				
Ser	Arg	Ser	Gln	Ser	Pro	Ser	Arg	Asp	Asp	Thr	Ser	Ser	Ser	Ser	Gly
						305		310			315			320	
His	Ser	Ser	Val	Asp	Thr	Ile	Pro	Phe	Phe	Ser	Glu	Asn	Leu	Pro	Ile
						325			330			335			
Gly	Glu	Leu	Phe	Ser	Tyr	Val	Asp	Pro	Leu	Thr	His	Ala	Leu	Phe	Ser
						340			345			350			
Ala	Cys	Thr	Thr	Leu	His	Val	Gly	Val	Gln	Leu	Leu	Arg	Glu	Asn	Glu
						355			360			365			
Ile	Thr	Leu	Gly	Val	His	Ser	Ala	Gln	Gly	Ile	Ala	Ala	Ser	Ile	Ser
						370			375			380			
Met	Ser	Gly	Glu	Pro	Gly	Glu	Asp	Ile	Ala	Arg	Thr	Gly	Ala	Thr	Asn
						385		390			395			400	
Ser	Thr	Arg	Cys	Glu	Glu	Gln	Pro	Thr	Thr	Pro	Ala	Ala	Arg	Val	Leu
						405			410			415			

Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 59
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 59
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Ile Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Gln Val Pro Ser Gln Ser Leu Ser Leu Asp Ile Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Gly

305	310	315	320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile			
325	330	335	
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser			
340	345	350	
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu			
355	360	365	
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser			
370	375	380	
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn			
385	390	395	400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu			
405	410	415	
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala			
420	425	430	
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp			
435	440	445	
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu			
450	455	460	
Asn Asn Ile Pro Pro			
465			

<210> 60

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 60

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro			
1	5	10	15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg			
20	25	30	
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn			
35	40	45	
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly			
50	55	60	
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln			
65	70	75	80
Ser Arg Ala Ala Asn Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His			
85	90	95	
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser			
100	105	110	
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp			
115	120	125	
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Phe Asp			
130	135	140	
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln			
145	150	155	160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val			
165	170	175	
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala			
180	185	190	
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu			
195	200	205	

Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Ile Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Ile Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Tyr Ile Ser
 370 375 380
 Lys Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 61
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 61
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Ile Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Arg Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Arg Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser

100	105	110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp		
115	120	125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp		
130	135	140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln		
145	150	155
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val		
165	170	175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala		
180	185	190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu		
195	200	205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu		
210	215	220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu		
225	230	235
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr		
245	250	255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys		
260	265	270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu		
275	280	285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly		
290	295	300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly		
305	310	315
His Ser Cys Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile		
325	330	335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser		
340	345	350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Tyr Glu		
355	360	365
Ile Thr Leu Gly Ile His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser		
370	375	380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn		
385	390	395
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu		
405	410	415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala		
420	425	430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp		
435	440	445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu		
450	455	460
Asn Asn Ile Pro Pro		
465		

<210> 62
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 62

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Ile Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Leu Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Asp Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Leu Gly Glu Asp Ile Val Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Ser Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu

450	455	460
Asn Asn Ile Pro Pro		
465		
<210> 63		
<211> 469		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> synthetically generated variant		
<400> 63		
Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro		
1 5 10 15		
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg		
20 25 30		
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn		
35 40 45		
Lys Glu Val Asn Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly		
50 55 60		
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln		
65 70 75 80		
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His		
85 90 95		
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Ile Ser		
100 105 110		
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp		
115 120 125		
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Ile Asp Glu Ala Ile Asp		
130 135 140		
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln		
145 150 155 160		
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val		
165 170 175		
Glu Lys Ala Pro Leu Pro Pro Ile Ser Ser Asp Ile Ala Arg Ala Ala		
180 185 190		
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu		
195 200 205		
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu		
210 215 220		
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu		
225 230 235 240		
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr		
245 250 255		
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys		
260 265 270		
Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu		
275 280 285		
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly		
290 295 300		
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly		
305 310 315 320		
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile		
325 330 335		
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser		
340 345 350		

Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 64

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 64

Met Ala Ala Glu Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Ile Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Glu Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Lys Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Thr Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr

	245	250	255
Leu Asp Glu Cys	Leu Arg Thr Lys Asn	Leu Phe Thr Ala Val His	Cys
260	265	270	
Tyr Ile Leu Asp Val Arg	Ile Leu Thr Ala Ile Ser	Glu Leu Leu Leu	
275	280	285	
Ser Gln Ile Arg Arg Thr	Gln Asn Ser His Met	Ser Pro Leu Glu Gly	
290	295	300	
Ser Arg Ser Gln Ser	Pro Ser Arg Asp Asp	Thr Ser Ser Ser Ser	Gly
305	310	315	320
His Ser Ser Val Asp	Thr Ile Pro Phe Ser	Glu Asn Leu Pro Ile	
325	330	335	
Gly Glu Leu Phe Ser Tyr Val Asp	Pro Leu Arg His Ala	Leu Phe Ser	
340	345	350	
Ala Cys Thr Thr Leu His Val	Gly Val Gln Leu Leu Arg	Glu Ile Glu	
355	360	365	
Ile Thr Leu Gly Val His Ser	Ala Arg Gly Ile Ala	Ala Ser Ile Ser	
370	375	380	
Met Ser Gly Glu Pro Gly	Glu Asp Ile Ala Arg	Thr Gly Ala Thr Asn	
385	390	395	400
Ser Ala Arg Cys Glu Glu Gln	Pro Thr Thr Pro Ala	Ala Arg Val Leu	
405	410	415	
Phe Met Phe Leu Ser Asp	Glu Gly Thr Phe Gln	Glu Ala Lys Ser Ala	
420	425	430	
Gly Ser Arg Gly Arg Thr	Ile Ala Ala Leu Arg Arg	Cys Tyr Glu Asp	
435	440	445	
Ile Phe Ser Leu Ala Arg	Lys His Lys His Gly	Met Leu Arg Asp Leu	
450	455	460	
Asn Asn Ile Pro Pro			
465			

<210> 65

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 65

Met Ala Ala Asp Gln Gly	Ile Phe Thr Asn Ser Val	Thr Leu Ser Pro	
1	5	10	15
Val Glu Gly Ser Arg Thr	Gly Gly Thr Leu Pro	Arg Arg Ala Phe Arg	
20	25	30	
Arg Ser Cys Asp Arg Cys	His Ala Gln Lys Ile	Lys Cys Thr Gly Asn	
35	40	45	
Lys Glu Val Thr Gly Arg	Ala Pro Cys Gln Arg	Cys Gln Gln Ala Gly	
50	55	60	
Leu Arg Cys Val Tyr Ser	Glu Arg Cys Pro Lys	Arg Lys Leu Arg Gln	
65	70	75	80
Ser Arg Ala Ala Asp	Leu Val Ser Ala Asp	Pro Asp Pro Cys Leu His	
85	90	95	
Met Ser Ser Pro Pro Val	Pro Ser Gln Ser Leu	Pro Leu Asp Val Ser	
100	105	110	
Glu Ser His Ser Ser Asn	Thr Ser Arg Gln Phe	Leu Asp Pro Pro Asp	
115	120	125	
Ser Tyr Asn Trp Leu Trp	Thr Ser Ile Gly Thr	Asp Glu Ala Ile Asp	
130	135	140	

Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Gly Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Gly Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 66
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 66
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 cgcaccggtg gaacattacc cccgggtgca ttccgacgct cttgtgatcg gtgtcatgca 120
 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
 tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgcacat gtcctcgcc 300

ccagtccct cacagagctt gccgctagac gtatccgagt cgcatccctc aaatacctcc 360
 cggcaggttc ttgatccacc ggacagctac gactgtcggt ggacctcgat tggcaactgac 420
 gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggcgt cagctgtcag 480
 ttagagccaa cgctgccgaa tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatcgagcga cattgctcggt gcggccagtg cgcaacgaga gctttcgat 600
 gacctgtcggt cggtgtcgca ggaacttgaa gagatccctc tggccgtgac ggtagaatgg 660
 ccaaaggcagg aaatctggac ccatcccatc ggaatgttt tcaatgcgtc acgacggcgtt 720
 cttactgtcc tgcgccaaca agcgcaggcc gactgccgtc aaggcacact agacgaatgt 780
 ttacggacca agaacctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
 accgccatat cggagttgtc cctgtcgcaaa attagcggaa cccagaacag ccatatgagc 900
 ccactggaag ggagtgcgtc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
 cacagcagtg ttgacaccat acccttctt agcgagaacc tccctattgg tgagctgttc 1020
 ccctatgttg accccctgac acacgcccata ttctcggtt gcactacgtt acatgttggg 1080
 gtacaattgc tgcgtgagaa tgagattact ctgggagttc actccgccc gggcattgca 1140
 gctccatca gcatgagcgg ggaaccaggc gaggatatacg ccaggacagg ggcgaccaat 1200
 tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttctt 1260
 agtcatgtcgg gggctttcca ggaggcaaag tctgtcggtt cccgaggcgt aaccatcgca 1320
 gcaactgcgtc gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 67
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 67
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 cgcaccgggtg gaacattacc ccggccgtgca ttccgacgt ctgtgtatcg gtgtcatgca 120
 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtatcg cgtctacagt gagcgtatgcc ccaagcgc当地 gctacgc当地 240
 tccagggcag cggatctcggt ctctgtcgac ccagatccct gcttgcacat gtcctcgct 300
 ccagtccct cacagagctt gccgctagac gtatccgagt cgcatccctc aaatacctcc 360
 tggcaatttc ttgatccacc ggacagctac gactgttgcgtt ggacctcgat tggcaactgac 420
 gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggcgt cagctgtcag 480
 ttagagccaa cgctgccgaa tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatcgagcga cattgctcggt gcggccagtg cgcaacgaga gctttcgat 600
 gacctgtcggt cggtgtcgca ggaacttgaa gagatccctc tggccgtgac ggttagagtgg 660
 ccaaaggcagg aaatctggac ccatcccatc ggaatgttt tcaatgcgtc acgacggcgtt 720
 cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
 ttacggacca agaacctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
 accgccatat cggagttgtc cctgtcgcaaa attagcggaa cccagaacag ccatatgagc 900
 ccactggaag ggagtgcgtc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
 cacggcagtg ttgacaccat acccttctt agcgagaacc tccctattgg tgagctgttc 1020
 tcctatgttg accccctgac acacgcccata ttctcggtt gcactacgtt acatgttggg 1080
 gtacaattgc tgcgtgagaa tgagattact ctgggagttc actccgccc gggcattgca 1140
 gctccatca gcatgagcgg ggaaccaggc gaggatatacg ccaggacagg ggcgaccaat 1200
 tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttctt 1260
 agtcatgtcgg gggctttcca ggaggcaaag tctgtcggtt cccgaggcgt aaccatcgca 1320
 gcaactgcgtc gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 68
 <211> 1410
 <212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 68

atggctgcag atcaaggtat attcacgaac tcggtcactc tctgccagt ggagggttca 60
 cgcacccgtg gaacattacc ccggcgtgca ttccgacgct ttgtgtatcg gtgtcatgca 120
 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtat cgctacagt gagcgcacgccc ccaagcgcaa gctacgccaa 240
 tccagggtag cggatctcgat ctctgctgac ccagatccct gttgcacat gtcctcgct 300
 ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactggctgt ggatctcgat tggcactgac 420
 gaggttattt acactgactg ctggggctgt tcccaatgtg atggagggtt cagctgtcag 480
 ttagagccaa cgctgcggat tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatcgagcga cattgctcgat gcccgcaggcg cgcaacgaga gctttcgat 600
 gacctgtcgat cgggtgcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccatcccattt ggaatgtttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcgcacaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
 ttacggacca agaaccttta tacggcagta cacttttaca tattgtatgt gcccgtttt 840
 accgccccat cggagttgtt cctgtcgcaaa attaggcgaa cccagaacacg ccatatgagc 900
 ccactggaaag ggagtgcgtt ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
 cacagcgttgc ttgacaccat acccttctt agcgagaacc tcccttattgg tgagctgttc 1020
 tcctatgttgc accccctgac acacggccctt ttctccgtt gcaactacgtt acatgttggg 1080
 gtacaatttgc tgcgtgagaa tgagattact ctggggatgtc actccggccca gggcatttgc 1140
 gcttccatca gcatgagcgg ggaaccaggc gaggatatacg ccaggacagg ggcgaccaat 1200
 tccgcaagat gcgaggagca gccgaccact ccagccgcgtt gggtttgcatgttctt 1260
 agtgtatgttgc gggcttccaa ggaggcaaaat tctgtgttgc cccgagggttgc aaccatcgca 1320
 gcactgcgac gatgtatgttgc ggtatctt tccctcgccc gcaaacacaaa acatggcatg 1380
 ctcagagacc tcaacaat tccctccatga 1410

<210> 69

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 69

atggctgcag atcaaggtat attcacgaac tcggtcactc tctgccagt ggagggttca 60
 cgcacccgtg gaacattacc ccggcgtgca ttccgacgct ttgtgtatcg gtgtcatgca 120
 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtat cgctacagt gagcgcacgccc ccaagcgcaa gctacgccaa 240
 tccagggtag cggatctcgat ctctgctgac ccagatccct gttgcacat gtcctcgct 300
 ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctcgat tggcactgac 420
 gaggttattt acactgactg ctggggctgt tcccaatgtg atggagggtt cagctgtcag 480
 ttagagccaa cgctgcggat tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatcgagcga cattgctcgat gcccgcaggcg cgcaacgaga gctttcgat 600
 gacctgtcgat cgggtgcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccatcccattt ggaatgtttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcgcacaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
 ttacggacca agaaccttta tacggcagta cacttttaca tattgtatgt gcccgtttt 840
 accgccccat cggagttgtt cctgtcgcaaa attaggcgaa cccagaacacg ccatatgagc 900
 ccactggaaag ggagtgcgtt ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
 cacagcgttgc ttgacaccat acccttctt agcgagaacc tcccttattgg tgagctgttc 1020

tccttatgtt accccctgac acacgcctta ttctcggtt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagttac actccgccc gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaa 1200
tccgcaagat gcgaggagca gccgaccact ccagcggtc gggtttgtt catgttctt 1260
agtgtatgaa gggctttcca ggaggcaaaag tctgtctgggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgttatgtt ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

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<210> 70
<211> 1410
<212> DNA
<213> Artificial Sequence
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<220>
<223> synthetically generated variant

<400> 70
atggctgcag atcaaggat attcacgaac tcggtcactc ttcgcgcagt ggagggttca 60
cgcacccgtg gaacattacc ccgcgcgtca ttccgacgc cttgtatcg gtgtcatgca 120
caaaaagatca aatgtactgg aaataaggag gtactggcc gtgcctccgt tcagcgttgc 180
cagcaggctg gacttcgtat cgtctacagt gagcgcacgc ccaagcgcaa gtcacgccaa 240
tccagggcag cgatctcgat ctctgtcgac ccagatccct gttgcacat gtcctcgcc 300
ccagtgccct cacagagctt gccgctagac gtatcccgat cgcattccctc aaatacctcc 360
cgccaatttc ttgatccacc ggacagctac gactggcgtg ggacctcgat tggactgac 420
gaggctattg acactgactg ctggggctg tcccaatgtg atggaggctt cagctgtcag 480
tttagagccaa cgctgcccga tctacccatcg cccttcgagat ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgtcgat gcccgcgtg cgcacacgaga gctttcgat 600
gacctgtcgg cgggtgcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaaccttta tacggcagta cactgttaca tattgaatgt gcggttttg 840
accgccccat cggagttgtc cctgtcgaa attaggcggg cccagaacacg ccatatgagc 900
ccactggaaag ggagtgcgtc ccagtgcgg agcagagacg acaccagcag cagcagcggc 960
cacagcgttgc ttgacaccat acccttctt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgttgc accccctgac acacgcctta ttctcggtt gcaactacgtt acatgttggg 1080
gtacaatttgc tgcgtgagaa tgagattact ctgggggtac actccgccta gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatacg ccaggacagg ggcgaccaat 1200
tcggcaagat gcgaggagca gccgactact ccagcggctc gggttttgtt catgttcttgc 1260
agtgtatgaag gggctttcca ggaggcggaaatg tctgtcggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgtatgttgc ggtatcttccctcgcc gcaaaacacaa acatggcatg 1380
ctcagagacc tcaacaatatttc tcctccatga 1410

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<210> 71
<211> 1410
<212> DNA
<213> Artificial Sequence
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<220>
<223> synthetically generated variant

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<400> 71
atggctgcag atcaaggat attcacgaac tcggtcactc tctcgccagt ggagggttca 60
cgcaccggtg gaacattacc ccgcccgtca ttccgacgct ctgtgtatcg gtgtcatgca 120
caaaaagatca aatgtactgg aaataaggag ttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccaggccag cgatctcgat ctctgctgac ccagatccct gcttgcacat gtcctcgccct 300
ccagtgcctc cacagagctt gccgctagac gtatccgagt cgcatccctc aaataccctcc 360
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cgccaatttc ttgatccacc ggacagctac gactggcgt ggacctcgat tggactgac 420
gaggctattg acactgactg ctggggcgt tcccaatatg atggaggct cagctgtcag 480
tttagccaa cgctgcccga tctacccctcg cccttcgagt ctacggtga aaaagctccg 540
ttgccaccgg tattcgagcga cattgctcgt gggccagtg cgcaacgaaa gctttcgat 600
gacctgtcgg cgggtgtcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgttt tcaatcggtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgcccattc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
gcccgcataat cgaggttgct cctgtcgaa attaggcggg cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttctt agcgagaacc tccctattgg tgagctgttc 1020
tcctatgtt accccctgac acacgcccata ttctcggtt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagttac actccgccta gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccata 1200
tccgcgaatgt gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgtatgtt gggctttcca ggaggcataag tctgtgtgtt cccgaggtcg aaccatcgca 1320
gcactgcccac gatgtatgtt ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

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<210> 72

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 72

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cgcaccggtg gaacattacc ccggcggtca ttccgacgt cttgtatcg gtgtcatgca 120
caaaaatca aatgtactgg aaataaggag gttactggcc gtgcctcctg tcagcgttgc 180
cagcaggctg gacttcgtat cgtctacagt gagcgcacgcc ccaagcgcaa gctacgccaa 240
tccagggcag cgatctcgat ctctgtcgac ccagatccct gttgcacat gtcctcgct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcatccctc aaataccctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctg ggacctcgat tggcaactgac 420
gaggctattg acaactgactg ctggggctg tcccaatgtt atggaggctt cagctgtcag 480
tttagagccaa cgctgcggta tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgtcgat gcccgcagg cgcaacgaga gctttcgat 600
gacctgtcgg cgggtgtcgca ggaactggaa gagatccccc tggccgtgac gtagaaatgg 660
ccgaaggcagg aaatctggac ccattccatc ggaatgttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcgcact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggttatttg 840
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gcactgcgac gatgtatgatggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacagttat tccctccatga 1410

<210> 73

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 73

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 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtat cgctacagt gagcgaacgccc ccaagcgcaa gctacgccaa 240
 tccagggcag cggatctcgat ttctgtcgac ccagatccct gcttgcacat gtcctcgcc 300
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 cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggactgac 420
 .gtgctattt gactgtactg ctggggctg tcccaatgtg atggaggctt cagctgtcag 480
 ttagagccaa cgctgcggta tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatcgagcga cattgtcgat gccggccatg cgcaacgaga gctttcgat 600
 gacctgtcg 720
 ccgaaggcagg aaatctggac ccatccatc ggaatgttt tcaatgcgtc acgacggctt 720
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 gcactgcgac gatgtatgtt ggtatctt tccctcgccc gcaaacacaaa acatggcatg 1380
 ctcagagacc tcaacaatata tccctccatgt 1410

<210> 74

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 74

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 caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtat cgctacagt gagcgaacgccc ccaagcgcaa gctacgccaa 240
 tccagggcag cggatctcgat ttctgtcgac ccagatccct gcttgcacat gtcctcgcc 300
 ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcatccctc aaatacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggactgac 420
 gaggttattt gactgtactg ctggggctg tcccaatgtg atggaggctt cagctgtcag 480
 ttagagccaa cgctgcggta tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
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 gacctgtcg 720
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 agtcatgaaag gggcttcca ggaggcaaag tctgctgggtt cccgaggctg aaccatcgca 1320
 gcaactgcac gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 75
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 75
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 cgcaccggtg gaacattacc ccggcgtgca ttccgacgct ttgtgtatcg gtgtcatgca 120
 aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtatcg cgtctacagt gagcgtatgcc ccaagcgc 240
 tccagggcag cggatctcgat ctctgctgac ccagatccct gcttgcacat gtcctcgct 300
 ccaagtgcct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactgtcgat gacactcgat tggcactgac 420
 gaggttattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtc 480
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 ccgaaggcagg aaatctggac ccatccatc ggaatgttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcccaaca agcgcaggcc gactgccatc aaggcacact agacaaatgt 780
 ttacggacca agaacctctt tacggcagta cacttttaca tattgtatgt gcccattttg 840
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 gcaactgcac gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 76
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 76
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 cgcaccgtg gaacattacc ccggcgtgca ttccgacgct ttgtgtatcg gtgtcatgca 120
 aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgtatcg cgtctacagt gagcgtatgcc ccaagcgc 240
 tccagggcag cggatctcgat ctctgctgac ccagatccct gcttgcacat gtcctcgct 300
 ccaagtgcct cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactgtcgat gacactcgat tggcactgac 420

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gacctgtcgg	cgggtgtcg	ggaactggaa	gagatccttc	tggccgtgac	ggtagaatgg	660
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cttactgtcc	tgcgccaaca	agcgcaggcc	gactgccatc	aaggcacact	agacgaatgt	780
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gtagaattgc	tgcgtgagaa	tgagattact	ctgggagttac	actccgccc	gggcattgca	1140
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tccgcaagat	gcgaggagca	gccgaccact	ccagcggctc	gggttttgtt	catgttcttg	1260
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ctcagagacc	tcaacaat	tcctccatga				1410

<210> 77
<211> 1410
<212> DNA
<213> Arti

<220>
<223> synthetically generated variant

<400> 77
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caaaagatca aatgtactgg aaataaggag gtactggcc gtgtccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgaa gctacgccc 240
tccaggccat cggatctcgat ctctgtcgac ccagatccct gcttgcacat gtcctcgcc 300
ccagtgcctc cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cgccaatttc ttgatccacc ggacagctac gactggcgtg ggacctcgat tggactgac 420
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agtgtatgaag gggctttcca ggaggcaaaag tctgtcggtt cccgaggtcg aaccatcaca 1320
gtactgcgac gaagctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
ctcaqagacc tcaacaatatt tccttcatga 1410

<210> 78
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 78

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 caaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
 tccaggggcag cggatctcgat cttctgtgac ccagatccct gcttgcacat gtcctcgct 300
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 cggcaatttc ttgatccacc ggacagctac gactggtcgt gacactcgat tggcactgac 420
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 ttgccaccgg tatcgagcga cattgctcgat gcccgcagtg cgcaacgaga gcttttcgat 600
 gacctgtcgg cgggtgtcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 cccgaaggcagg aaatctggac ccattccatc ggaatgttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcgcacaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
 ttacggacca agaaccttta tacggcagta cactgttaca tattgaatgt gcggttgg 840
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 gtacaattgc tgcgtgagaa ttagattact ctgggagttac actccgcctc gggcattgca 1140
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<210> 79

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 79

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 caaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
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 ttgccaccgg tatcgagcga cattgctcgat gcccgcagtg cgcaacgaga gcttttcgat 600
 gacctgtcgg cgggtgtcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 ccctaaggcagg aaatctggac ccattccatc ggaatgttt tcaatgcgtc acgacggctt 720
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gcactgcgac gatgttatgtt ggatatcttt tccctcgcccc gcaaacacaa atatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410
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<210> 80
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 80
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cagcaggctg gacttcgtat cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cgatctcgat ctctgctgac ccagatccct gttgcacat gtcctcgct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcatccctc aaatacctcc 360
cgccaatttc ttgatccacc ggacagctac gactggcgt ggacctcgat tggactgtac 420
gaggctattt gacactgactg ctgggggctg tcccaatgtt atggaggctt cagctgtcag 480
tttagagccaa cgctgcccggta tctacccctcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgat gcccggcgttgcgcaacgaga gctttcgat 600
gacctgtcgg cggtgtcgca ggaactggaa gagatccccc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaaccttta tacggcagta cactgttaca tattgaatgt gcggattttg 840
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gcactgcgac gatgtatgttgc gatgtatgttgc tccctcgcccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatataat tccctccatgtac 1410

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<210> 81
<211> 1410
<212> DNA
<213> Artificial Sequence
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<220>
<223> synthetically generated variant

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<400> 81
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cgcaccggtg gaacattacc ccgcccgtgca ttacgacgct ctgtgtatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgtccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgtcaa gttacgcctaa 240
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cgccaatttc ttgatccacc ggacagctac gactggctgt ggacactcgat tggcactgac 420
qaggctattq acactgactq ctqqqqqctq tcccaacqtq atqqaqqctt cagctctcaq 480
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ttaaagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
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 gacctgtcgg cgggtcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccattccatc ggaatgttt tcaatgcgtc acgacggctt 720
 cttaactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacaaatgt 780
 ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
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 ccacttggaaag ggagtcgatc ccagtcgccc aacagagacg acaccagcag cagcagccgc 960
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 gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgccc gggcattgca 1140
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 tccgcaagat gcgaggagca gocgaccact ccagccgtc gggttttgtt catgttctt 1260
 agtgtatgaag gggcttcca ggaggcaaaat tctgtcggtt cccgaggctg aaccatcgca 1320
 gcaactgcgac gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 82
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 82
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 cagcaggctg gacttcgtat cgtctacagt gagcgtatgcc ccaagcgc 240
 tccagggcag cggatctcgat ctctgtcgac ccagatccct gcttgcacat gtcctcgcc 300
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 cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctcgat ttgcactgac 420
 gaggctattt acactgactg ctggggctgt tcccaatgtt atggaggctt cagctgtc 480
 ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
 ttgccaccgg tatkagcga cattgctcggt gcggccagtg cgcaacgaga gctttcgat 600
 gacctgtcgg cgggtcgca ggaactggaa gagatccctc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccattccatc ggaatgttt tcaatgcgtc acgacggctt 720
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 agtgtatgaag gggcttcca ggaggcaaaat tctgtcggtt cccgaggctg aaccatcgca 1320
 gcaactgcgac gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatat tcctccatga 1410

<210> 83
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 83

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 caaaagatca aatgtactgg aaataaggag gttatggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
 tccagggcag cgatctcgat ctctgctgac ccagatccct gcttgcacat gtcctcgct 300
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 cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctcgat tggcaactgac 420
 gaggttattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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 ttgccaccgg tatacgacgca cattgctcgat gcccgcgtg cgcaacgaga gctttcgat 600
 gacctgtcgg cgggtgtcgca ggaacttgaa gagatccctc tggccgtgac ggtagaatgg 660
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 cttactgtcc tgcgcacaaca agcgcaggcc gactgccatc aaggcacact agacaaatgt 780
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 gcaactgcgac gatgctatga ggatatctt tccctcgccc gcaaacacaa acatggcatg 1380
 ctcagagacc tcaacaatataat tccctccatga 1410

<210> 84

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 84

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 caaaagatca aatgtactgg aaataaggag gttatggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
 tccagggcag cgatctcgat ctctgctgac ccagatccct gcttgcacat gtcctcgct 300
 ccagtgcctc cacagagctt gtcgctagac atatccgagt cgcattccctc aaataacctcc 360
 cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctcgat tggcaactgac 420
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 gacctgtcgg cgggtgtcgca ggaacttgaa gagatccctc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccatccatc ggaatgttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcgcacaaca agcgcaggcc gactgccatc aaggcacact agacaaatgt 780
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gcactgcgac gatgttatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410
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<210> 85
<211> 1410
<212> DNA
<213> Artificial Sequence
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<220>
<223> synthetically generated variant

<400> 85
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cgcacccgtg gaacattacc ccgcgcgtca ttccgacgc cttgtatcg gtgtcatgca 120
caaaaagatca aatgtactgg aaataaggag gtactggcc gtgcctccgt tcagcgttgc 180
cagcaggctg gacttcgtat cgtctacagt gagcgatgcc ccaagcgaa gctacgccaa 240
tccagggcag cgaatctcgat ctctgtgtcc ccaagatccct gcttacacat gtcctcgcc 300
ccagtgccct cacagagctt gccgctagac gtatcccgat cgcattcctc aaatacctcc 360
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gaggcttttgc acactgtactg ctgggggcta tcccaatgtt atggaggctt cagctgtcag 480
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gcactgcgac gatgtatgttgc ggtatctttt tccctcgccc gcaaaacacaa acatggcatg 1380
ctcagagacc tcaacaatattt tcctccatgtt 1410

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<210> 86
<211> 1410
<212> DNA
<213> Artificial Sequence
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<220>
<223> synthetically generated variant

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<400> 86
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cgcacccgtg gaacattacc ccgcgcgtca ttccgacgct ttgtgtatcg gtgtcatgca 120
caaaaagatca aatgtattgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
caacgggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgca gctacgcca 240
tccagggcag cgatctcgat ctctgcgtac ccagatccct gcttgcacat gtccctcgct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcatccctc aaatacctcc 360
cgccaatttc ttgatccacc ggacagctac gactggctgt ggacccgtat tggcaactgac 420
gaggctattg acactgactg ctggggctg tcccaatgtg atggaggctt cagctgtcag 480
tttagagccaa cgctgcggat tctacccctcg cccttcgagt ctacgggttga aaaagctccg 540
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 ccgaaggcagg aaatctggac ccatccatc ggaatgttt tcaatgcgtc acgacggctt 720
 cttactgtcc tgcgccaaca agctcaggcc gactgccatc aaggcacact agacgaatgt 780
 ttacggacca agaacctctt tacggcagta cactttaca tattgaatgt gcggattttg 840
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 ccacttggaa ggagtgcgtc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
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 ctcagagatc tcaacaatat tcctccatga 1410

<210> 87
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 87
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 cgaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagaagctg gacttcgtcgt cgtctatagt gagcgtatgcc ccaagcgc当地 gctacgc当地 240
 tccagggcag cggatctcgt ctctgtcgac ccagatccct gcttgcacat gtcctcgcc 300
 ccagtgc当地 cacagagctt gccgcttagac gtatccgagt cgcattccctc aaataccctcc 360
 cggcaatttc ttgatccacc ggacagctac gactggcgtt ggacctcgat tggcactgac 420
 gaggttattt acactgactg ctgggggctg tcccaatgtt atggaggctt cagctgtc当地 480
 ctagagccaa cgctgccc当地 tctaccttc当地 cccttc当地 gtc当地 ctacgggtt当地 aaaagctccg 540
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 gacctgtcg gggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
 ccgaaggcagg aaatctggac ccatccatc ggaatgttt tcaatgcgtc acgacggctt 720
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 ctcagagacc tcaacaatat tcctccatga 1410

<210> 88
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 88

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 caaaagatca aatgtactgg aaataaggag gttaatggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
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<210> 89

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 89

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 cgaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
 cagcaggctg gacttcgatg tttctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
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 ctcagagacc tcaacaatat tcctccatga 1410

<210> 90
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 90
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 caaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcggtgc 180
 cagcaggctg gacttcgtatcgat cgtctacagt gagcgtatgcc ccaagcgcaa gctacgccaa 240
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 gacccgtcgat cggatcgat gaaactggaa gagatccctc tggccgtgac ggtagaatgg 660
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 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
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Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln		
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Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val		
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Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala		
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Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu		
195	200	205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu		
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Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys		
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Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu		
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Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly		
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Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly		
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His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile		
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Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser		
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Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser		
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Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala		
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